

1 AAGTAAAAGAAAGAGCGAGAAATCATCGAAATGGATTCATCTCATCTCTTATCGTTGGC
 1 +-----+-----+-----+-----+-----+-----+ 60
 1 TTCATTTCTTCTCGCTCTTAGTAGCTTACCTAAAGTAGAGTAGAGAATAGCAACCG

 a K * K K E R E I I E (M) D F I S S L I V G -
 b S K R K S E K S S K W I S S H L L S L A -
 c V K E R A R N H R N G F H L I S Y R W L -

 61 TGTGCTCAGGTGTTGTGAATCTATGAATATGGCGGAGAGAAGAGGACATAAGACTGAT
 61 +-----+-----+-----+-----+-----+-----+ 120
 61 ACACGAGTCCACAACACACTTAGATACTTACCGCCTCTCTCCTGTATTCTGACTA

 a C A Q V L C E S M N M A E R R G H K T D -
 b V L R C C V N L * I W R R E E D I R L I -
 c C S G V V * I Y E Y G G E K R T * D * S -

 121 CTTAGACAAGCCATCACTGATCTTGAACAGCCATCGGTGACTTGAGGCCATACGTGAT
 121 +-----+-----+-----+-----+-----+-----+ 180
 121 GAATCTGTTCGGTAGTAGACTAGAACCTTGTGGTAGCCACTGAACCTCCGGTATGCACTA

 a L R Q A I T D L E T A I G D L K A I R D -
 b L D K P S L I L K Q P S V T * R P Y V M -
 c * T S H H * S * N S H R * L E G H T * * -

 181 GACCTGACTTTACGGATCCAACAAGACGGCTAGAGGGACGAAGCTGCTCAAATCGTGCC
 181 +-----+-----+-----+-----+-----+-----+ 240
 181 CTGGACTGAAATGCCTAGGTTGTTCTGCCAGATCTCCCTGTTGACGAGTTAGCACGG

 a D L T L R I Q Q D G L E G R S C S N R A -
 b T * L Y G S N K T V * R D E A A Q I V P -
 c P D F T D P T R R S R G T K L L K S C Q -

 241 AGAGAGTGGCTTAGTGCCTGGCAAGTAACGGAGACTAAAACAGCCCTACTTTAGTGAGG
 241 +-----+-----+-----+-----+-----+-----+ 300
 241 TCTCTACCGAATCACGCCACGTTCAATTGCCCTGATTTGTGGGATGAAATCACTCC

 a R E W L S A V Q V T E T K T A L L L V R -
 b E S G L V R C K * R R L K Q P Y F * * G -
 c R V A * C G A S N G D * N S P T F S E V -

 301 TTTAGGCGTCGGGAACAGAGGACGCGAATGAGGAGGAGATACCTCAGTTGTTCGGTTGT
 301 +-----+-----+-----+-----+-----+-----+ 360
 301 AAATCCGCAGCCCTTGTCTCCTGCGCTTACTCCTCCTATGGAGTCAACAAAGCCAACA

 a F R R R E Q R T R M R R R Y L S C F G C -
 b L G V G N R G R E * G G D T S V V S V V -
 c * A S G T E D A N E E E I P Q L F R L C -

 361 GCCGACTACAAACTGTGCAAGAAGGTTCTGCCATATTGAAGAGCATTGGTGAGCTGAGA
 361 +-----+-----+-----+-----+-----+-----+ 420
 361 CGGCTGATGTTGACACGTTCTCAAAGACGGTATAACTCTCGTAACCAACTCGACTCT

Fig. 2A

a	A D Y K L C K K V S A I L K S I G E L R -
b	P T T N C A R R F L P Y * R A L V S * E -
c	R L Q T V Q E G F C H I E E H W * A E R -
	GAACGCTCTGAAGCTATCAAAACAGATGGCGGGTCAATTCAAGTAACCTGTAGAGAGATA
421	-----+-----+-----+-----+-----+-----+-----+ 480
	CTTGCAGACTTCGATAGTTGTCTACCGCCCAGTTAACATCTCTAT
a	E R S E A I K T D G G S I Q V T C R E I -
b	N A L K L S K Q M A G Q F K * L V E R Y -
c	T L * S Y Q N R W R V N S S N L * R D T -
	CCCATCAAGTCCGTTGCGAAATACCACGATGATGGAACAGGTTGGAAATTTCAGT
481	-----+-----+-----+-----+-----+-----+-----+ 540
	GGGTAGTTCAAGCAACAGCCTTATGGTGCCTACTACCTGTCCAAAACCTTAAAGAGTCA
a	P I K S V V G N T T M M E Q V L E F L S -
b	P S S P L S E I P R * W N R F W N F S V -
c	H Q V R C R K Y H D D G T G F G I S Q * -
	GAAGAAGAAGAAAGAGGAATCATTGGTGTATGGACCTGGTGGGGTTGGGAAGACAACG
541	-----+-----+-----+-----+-----+-----+-----+ 600
	CTTCTTCTTCTCTCTTAGTAACCACAAATACCTGGACCACCCCAACCCTCTGTTGC
a	E E E E R G I I G V Y G P G G V G K T T -
b	K K K K E E S L V F M D L V G L G R Q R -
c	R R R K R N H W C L W T W W G W E D N V -
	TTAATGCAGAGCAATTAAACAACGAGCTGATCACAAAGGACATCAGTATGATGTACTGATT
601	-----+-----+-----+-----+-----+-----+-----+ 660
	AATTACGTCTCGTAATTGTTGCTCGACTAGTGTGTTCTGTAGTCATACTACATGACTAA
a	L M Q S I N N E L I T K G H Q Y D V L I -
b	* C R A L T T S * S Q K D I S M M Y * F -
c	N A E H * Q R A D H K R T S V * C T D L -
	TGGGTTCAAATGTCCAGAGAATTGGCGAGTGTACAATTCAAGCAAGCCGTTGGACCG
661	-----+-----+-----+-----+-----+-----+-----+ 720
	ACCCAAGTTACAGGTCTTAAGCCGCTCACATGTTAACATCGTTCGGCAACCTCGTGCC
a	W V Q M S R E F G E C T I Q Q A V G A R -
b	G F K C P E N S A S V Q F S K P L E H G -
c	G S N V Q R I R R V Y N S A S R W S T V -
	TTGGGTTTATCTTGGGACGAGAAGGGAGACCGGGAAAAACAGAGCTTGAAGATATAACAGA
721	-----+-----+-----+-----+-----+-----+-----+ 780
	AACCCAAATAGAACCTGCTTCCCTGGCCGTTTGTCTCGAAACCTCTATATGTCT
a	L G L S W D E K E T G E N R A L K I Y R -
b	W V Y L G T R R R P A K T E L * R Y T E -
c	G F I L G R E G D R R K Q S F E D I Q S -
	GCTTTGAGACAGAACGTTCTTGTGTTGCTAGATGATGTCTGGGAAGAGATAACTTG
781	-----+-----+-----+-----+-----+-----+-----+ 840
	CGAAACTCTGTCTTGCAAAGAACACAACGATCTACTACAGACCCCTCTATCTGAAC

Fig. 2B

a A L R Q K R F L L L D D D V W E E I D L -
 b L * D R N V S C C C * M M S G K R * T W -
 c F E T E T F L V V A R * C L G R D R L G -

 GAGAAAATGGAGTTCCTCGACCTGACAGGGAAAACAAATGCAAGGTGATGTTACGACA
 841 -----+-----+-----+-----+-----+-----+ 900
 CTCTTTGACCTCAAGGAGCTGGACTGTCCCTTTGTTACGTTCACTACAAGTGCTGT

 a E K T G V P R P D R E N K C K V M F T T -
 b R K L E F L D L T G K T N A R * C S R H -
 c E N W S S S T * Q G K Q M Q G D V H D T -

 CGGTCTATAGCATTATGCAACAATATGGGTGCGGAATACAAGTTGAGAGTGGAGTTCTG
 901 -----+-----+-----+-----+-----+-----+ 960
 GCCAGATATCGTAATACGTTATACCCACGCCCTATGTTCAACTCTCACCTCAAAGAC

 a R S I A L C N N M G A E Y K L R V E F L -
 b G L * H Y A T I W V R N T S * E W S F W -
 c V Y S I M Q Q Y G C G I Q V E S G V S G -

 GAGAAGAAAACACGCGTGGGAGCTGTTCTGTAGTAAGGTATGGAGAAAAGATTTAGAG
 961 -----+-----+-----+-----+-----+-----+ 1020
 CTCTTCTTGTGCGCACCCCTCGACAAGACATCATTCCATACCTCTTTCTAGAAAATCTC

 a E K K H A W E L F C S K V W R K D L L E -
 b R R N T R G S C S V V R Y G E K I F * S -
 c E E T R V G A V L * * G M E K R S F R V -

 TCATCATCAATTGCCGGCTCGGGAGATTATAGTAGTAAATGTGGAGGATTGCCACTA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 AGTAGTAGTTAACCGGCCGAGCGCTCTAATATCACTCATTACACCTCCTAACGGTGAT

 a S S S I R R L A E I I V S K C G G L P L -
 b H H Q F A G S R R L * * V N V E D C H * -
 c I I N S P A R G D Y S E * M W R I A T S -

 GCGTTGATCACTTAGGAGGCCATGGCTCATAGAGAGACAGAAGAAGAGTGGATCCAT
 1081 -----+-----+-----+-----+-----+-----+ 1140
 CGCAACTAGTGAATCCTCCTCGGTACCGAGTATCTCTGTCTTCTCACCTAGGTA

 a A L I T L G G A M A H R E T E E E W I H -
 b R * S L * E E P W L I E R Q K K S G S M -
 c V D H F R R S H G S * R D R R R V D P C -

 GCTAGTGAAGTTCTGACTAGATTCCAGCAGAGATGAAGGGTATGAACTATGTATTTGCC
 1141 -----+-----+-----+-----+-----+-----+ 1200
 CGATCACTTCAAGACTGATCTAAAGGTGCTCTACTTCCCATACTTGATACATAAACGG

 a A S E V L T R F P A E M K G M N Y V F A -
 b L V K F * L D F Q Q R * R V * T M Y L P -
 c * * S S D * I S S R D E G Y E L C I C P -

 CTTTGAAATTCACTACGACAACCTCGAGAGTGAATCTGCTTCGGTCTTGTAC
 1201 -----+-----+-----+-----+-----+-----+ 1260
 GAAAACTTAAGTCGATGCTGGAGCTCACTAGACGAAGCCAGAACAAAGAACATG

Fig. 2C

L K F S Y D N L E S D L L R S C F L Y -
 F * N S A T T T S R V I C F G L V S C T -
 F E I Q L R Q P R E * S A S V L F L V L -

1261 TCGCCTTATTCCAGAAGAACATTCTATAGAGATCGAGCAGCTGTTGAGTACTGGTC
 -----+-----+-----+-----+-----+-----+ 1320
 ACGCGAAATAAGGGTCTCTGTAAAGATATCTAGCTCGCAACAACTCATGACCCAG

C A L F P E E H S I E I E Q L V E Y W V -
 A L Y S Q K N I L * R S S S L L S T G S -
 R F I P R R T F Y R D R A A C * V L G R -

1321 GGCAGGGTTCTCACAGCTCCATGGCGTTAACACCATTACAAGGGATATTTCTC
 -----+-----+-----+-----+-----+-----+ 1380
 CGCCTCCCAAAGAGTGGTCGAGGGTACCGCAATTGTGGTAAATGTTCCCTATAAAAGAG

G E G F L T S S H G V N T I Y K G Y F L -
 A K G F S P A P M A L T P F T R D I F S -
 R R V S H Q L P W R * H H L Q G I F S H -

1381 ATTGGGGATCTGAAAGCGGCATGTTGTTGGAAACCGGAGATGAGAAAACACAGGTGAAG
 -----+-----+-----+-----+-----+-----+ 1440
 TAACCCCTAGACTTTCGCCGTACAAACAACCTTGGCCTCTACTCTTTGTGTCCACTTC

I G D L K A A C L L E T G D E K T Q V K -
 L G I * K R H V C W K P E M R K H R * R -
 W G S E S G M F V G N R R * E N T G E D -

1441 ATGCATAATGTGGTCAGAAGCTTGCAATTGTTGGATGGCATCTGAACAGGGACTTATAAG
 -----+-----+-----+-----+-----+-----+ 1500
 TACGTATTACACCAGTCTCGAAACGTAACACCTACCGTAGACTTGTCCCTGAATATTTC

M H N V V R S F A L W M A S E Q G T Y K -
 C I M W S E A L H C G W H L N R G L I R -
 A * C G Q K L C I V D G I * T G D L * G -

1501 GAGCTGATCCTAGTTGAGCCTAGCATGGACATACTGAAGCTCCTAAAGCAGAAAAGTGG
 -----+-----+-----+-----+-----+-----+ 1560
 CTCGACTAGGATCAACTCGGATCGTACCTGTATGACTTCGAGGATTCTGTCTTTGACC

E L I L V E P S M G H T E A P K A E N W -
 S * S * L S L A W D I L K L L K Q K T G -
 A D P S * A * H G T Y * S S * S R K L A -

1561 CGACAAGCGTTGGTGATCTCATTGTTAGATAACAGAACCTGCCTGAAAAACTC
 -----+-----+-----+-----+-----+-----+ 1620
 GCTGTTCGCAACCACTAGAGTAACAATCTATTGTCTTAGGTCTGGAACGGACTTTTGAG

R Q A L V I S L L D N R I Q T L P E K L -
 D K R W * S H C * I T E S R P C L K N S -
 T S V G D L I V R * Q N P D L A * K T H -

Fig. 2D

ATATGCCGAAACTGACAACACTGATGCTCCAACAGAACAGCTTTGAAGAAGATTCCA
 1621 -----+-----+-----+-----+-----+-----+ 1680
 TATAACGGGCTTGTGACTGTTGTGACTACGAGGTTGTCTTGTGAGAAACTTCTTAAGGT

a	I C P K L T T L M L Q Q N S S L K K I P -
b	Y A R N * Q H * C S N R T A L * R R F Q -
c	M P E T D N T D A P T E Q L F E E D S N -

ACAGGGTTTCATGCATATGCCTGTTCTCAGAGTCTGGACTTGTGTTACAGTATC
 1681 -----+-----+-----+-----+-----+ 1740
 TGTCACAAAAGTACGTATAACGGACAAGAGTCTCAGAACCTGAACAGCAAGTGTTCATAG

a	T G F F M H M P V L R V L D L S F T S I -
b	Q G F S C I C L F S E S W T C R S Q V S -
c	R V F H A Y A C S Q S L G L V V H K Y H -

ACTGAGATTCCGTTGTCTATCAAGTATTGGTGGAGTTGTATCATCTGTCTATGTCAGGA
 1741 -----+-----+-----+-----+-----+ 1800
 TGACTCTAAGGCAACAGATAGTCATAAACACCCTCAACATAGTAGACAGATACTGCT

a	T E I P L S I K Y L V E L Y H L S M S G -
b	L R F R C L S S I W W S C I I C L C Q E -
c	* D S V V Y Q V F G G V V S S V Y V R N -

ACAAAAGATAAGTGTATTGCCACAGGAGCTTGGGAATCTTAGAAAAGTGAAGCATCTGGAC
 1801 -----+-----+-----+-----+-----+ 1860
 TGTTTCTATTCACATAACGGTGTCTCGAACCCCTAGAATCTTGTGACTTCGTAGACCTG

a	T K I S V L P Q E L G N L R K L K H L D -
b	Q R * V Y C H R S L G I L E N * S I W T -
c	K D K C I A T G A W E S * K T E A S G P -

CTACAAAGAACTCAGTTCTCAGACGATCCCACGAGATGCCATATGTTGGCTGAGCAAG
 1861 -----+-----+-----+-----+-----+ 1920
 GATGTTTCTTGAGTCAAAGAAGTCTGCTAGGGTGTCTACGGTATACAACCGACTCGTTC

a	L Q R T Q F L Q T I P R D A I C W L S K -
b	Y K E L S F F R R S H E M P Y V G * A S -
c	T K N S V S S D D P T R C H M L A E Q A -

CTCGAGGTTCTGAACCTGTACTACAGTTACGCCGGTTGGGAACAGCAGCTTGGAGAA
 1921 -----+-----+-----+-----+-----+ 1980
 GAGCTCCAAGACTTGAACATGATGTCAATGCCAACCTTGACGTCTCGAACCTCTT

a	L E V L N L Y Y S Y A G W E L Q S F G E -
b	S R F * T C T T V T P V G N C R A L E K -
c	R G S E L V L Q L R R L G T A E L W R R -

GATGAAGCAGAAGAACTCGGATTGCTGACTTGGAAACTTGGAAAACCTAACCAACTC
 1981 -----+-----+-----+-----+-----+ 2040
 CTACTTCGTCTTCTGAGCCTAACGCGACTGAACCTTATGAACCTTTGGATTGGTGTGAG

Fig. 2E

a D E A E E L G F A D L E Y L E N L T T L -
 b M K Q K N S D S L T W N T W K T * P H S -
 c * S R R T R I R * L G I L G K P N H T R -

 GGTATCACTGTTCTCTCATTGGAGACCTAAAAACTCTCTCGAGTTGGTGCCTTCAT
 2041 -----+-----+-----+-----+-----+-----+ 2100
 CCATAGTGACAAGAGAGTAACCTCTGGGATTTGAGAGAAGCTAACGCCACGAAACGTA

 a G I T V L S L E T L K T L F E F G A L H -
 b V S L F S H W R P * K L S S S S S V L C I -
 c Y H C S L I G D P K N S L R V R C F A * -

 AAACATATAACAGCATCTCCACGTTGAAGAGTGCAATGAACTCCTACTTCAATCTCCC
 2101 -----+-----+-----+-----+-----+-----+ 2160
 TTTGTATATGTCGTAGAGGTGCAAACCTCTCACGTTACTTGAGGAGATGAAGTTAGAGGGT

 a K H I Q H L H V E E C N E L L Y F N L P -
 b N I Y S I S T L K S A M N S S T S I S H -
 c T Y T A S P R * R V Q * T P L L Q S P I -

 TCACTCACTAACCATGGCAGGAACCTGAGAAGACTTAGCATTAAAAGTTGCCATGACTTG
 2161 -----+-----+-----+-----+-----+-----+ 2220
 AGTGAGTGATTGGTACCGTCCTGGACTCTCTGAATCGTAATTCAACGGTACTGAAC

 a S L T N H G R N L R R L S I K S C H D L -
 b H S L T M A G T * E D L A L K V A M T W -
 c T R * P W Q E P E K T * H * K L P * L G -

 GAGTACCTGGTCACACCCGCAGATTTGAAAATGATTGGCTTCCAGTCTAGAGGTTCTG
 2221 -----+-----+-----+-----+-----+-----+ 2280
 CTCATGGACCAGTGTGGCGTCTAAACTTTACTAACCGAAGGCTCAGATCTCCAAGAC

 a E Y L V T P A D F E N D W L P S L E V L -
 b S T W S H P Q I L K M I G F R V * R F * -
 c V P G H T R R F * K * L A S E S R G S D -

 ACGTTACACAGCCTTCACAACCTAACCGAGTGTTGGGAAATTCTGTAAGCCAAGATTGT
 2281 -----+-----+-----+-----+-----+-----+ 2340
 TGCAATGTGTCGGAAGTGTGAATTGGTCTCACACCCCTTAAGACATTGGTCTAACAC

 a T L H S L H N L T R V W G N S V S Q D C -
 b R Y T A F T T * P E C G E I L * A K I V -
 c V T Q P S Q L N Q S V G K F C K P R L S -

 CTGCGGAATATCCGTTGCATAAACATTTACACTGCAACAAGCTGAAGAATGTCTCATGG
 2341 -----+-----+-----+-----+-----+-----+ 2400
 GACGCCTTATAGGCAACGTATTGTAAGTGTGACGTTGTCACCTTACAGAGTACCA

 a L R N I R C I N I S H C N K L K N V S W -
 b C G I S V A * T F H T A T S * R M S H G -
 c A E Y P L H K H F T L Q Q A E E C L M G -

 GTTCAGAAACTCCCAAAGCTAGAGGTGATTGAACTGTTGACTGCCAGAGAGATAGAGGAA
 2401 -----+-----+-----+-----+-----+-----+ 2460
 CAAGTCTTGAGGGTTGATCTCCACTAACCTGACAAGCTGACGTCTCTATCTCCTT

Fig. 2F

a V Q K L P K L E V I E L F D C R E I E E -
 b F R N S Q S * R * L N C S T A E R * R N -
 c S E T P K A R G D * T V R L Q R D R G I -

 TTGATAAGCGAACACGAGAGTCATCCGTCGAAGATCCAACATTGTTCCAAGCCTGAAG
 2461 -----+-----+-----+-----+-----+-----+ 2520
 AACTATTGCTTGTGCTCTCAGGTAGGCAGCTTAGGTTGTAACAAGGGTTCGGACTTC

 a L I S E H E S P S V E D P T L F P S L K -
 b * * A N T R V H P S K I Q H C S Q A * R -
 c D K R T R E S I R R R S N I V P K P E D -

 ACCTTGAGAACTAGGGATCTGCCAGAACTAAACAGCATCCTCCCATCTCGATTTCATTC
 2521 -----+-----+-----+-----+-----+-----+ 2580
 TGGAACCTTGATCCCTAGACGGTCTGATTGTCGTAGGAGGGTAGAGCTAAAAGTAAG

 a T L R T R D L P E L N S I L P S R F S F -
 b P * E L G I C Q N * T A S S H L D F H S -
 c L E N * G S A R T K Q H P P I S I F I P -

 CAAAAAGTTGAAACATTAGTCATCACAAATTGCCAGAGTTAAGAAACTGCCGTTTCAG
 2581 -----+-----+-----+-----+-----+-----+ 2640
 GTTTTCAACTTGTAAATCAGTAGTGTAAACGGGCTCTAATTCTTGACGGCAAAGTC

 a Q K V E T L V I T N C P R V K K L P F Q -
 b K K L K H * S S Q I A P E L R N C R F R -
 c K S * N I S H H K L P Q S * E T A V S G -

 GAGAGGAGGACCCAGATGAACTTGCCAACAGTTATTGTGAGGAGAAATGGTGGAAAGCA
 2641 -----+-----+-----+-----+-----+-----+ 2700
 CTCTCCTCCTGGGTCTACTTGAACGGTGTCAAATAACACTCCTCTTACCACCTTCGT

 a E R R T Q M N L P T V Y C E E K W W K A -
 b R G G P R * T C Q Q F I V R R N G G K H -
 c E E D P D E L A N S L L * G E M V E S T -

 CTGGAAAAAGATCAACCAACGAAGAGCTTGTATTACCGCGTTGTTCAAATTGA
 2701 -----+-----+-----+-----+-----+-----+ 2760
 GACCTTTCTAGTTGGTTGCTCTCGAAACAATAATGGCGCAAACAAGGTTAACT

 a L E K D Q P N E E L C Y L P R F V P N * -
 b W K K I N Q T K S F V I Y R A L F Q I D -
 c G K R S T K R R A L L F T A L C S K L I -

 TATAAGAGCTAAGAGCACTCTGTACAAATATGCCATTATAAGATGCAGGAAGCCAGGA
 2761 -----+-----+-----+-----+-----+-----+ 2820
 ATATTCTCGATTCTCGTGAGACATGTTATACAGGTAAAGTATTCTACGTCTCGGTCT

 a Y K S * E H S V Q I C P F I R C R K P G -
 b I R A K S T L Y K Y V H S * D A G S Q E -
 c * E L R A L C T N M S I H K M Q E A R K -

 AGGTTGTTCCAGTGAAGTCATCAACTTCCACATAGCCACAAAAGTAGAGATTATGTAAT
 2821 -----+-----+-----+-----+-----+-----+ 2880
 TCCAACAAGGTCACTTCAGTAGTTGAAAGGTGTATCGGTGTTGATCTAATACATTA

Fig. 2G

a R L F Q * S H Q L S T * P Q N * R L C N -
b G C S S E V I N F P H S H K T R D Y V I -
c V V P V K S S T F H I A T K L E I M * S -

CATAAAAACCAAACATATCCCGCA
2881 -----+-----+--- 2903
GTATTTTGGTTTGATAGGCGCT

a H K N Q T I R -
b I K T K L S A -
c * K P N Y P R -

ENZYMES THAT DO CUT:

NONE

ENZYMES THAT DO NOT CUT:

KpnI

Fig. 2H

-146 ATCGATTGATCTCTGGCTCAGTGCAGTAGTCCTTGAGAGCAGTCGTAGCCCCGCGTG -86
 GCGCATCATGGAGCTATTGGAATTTCGCAGGGTTATCGATTGAGTAGGGAAACCCATT -26
 CATTGTTGGAACCACCAACGGACGACTTAACAAGCTCCCCGAGGTGATGATGAAAATT 35
 MetLysIle
 AlaProValAlaIleAsnHisSerProLeuSerArgGluValProSerHisAlaAlaPro
 GCTCCAGTTGCCATAAATCACAGCCCGCTCAGCAGGGAGGTCCCGTCACACGGGCACCC 95
 AlaProValAlaIleAsnHisSerProLeuSerArgGluValProSerHisAlaAlaPro
 ACTCAGGCAAAGCAAACCAACCTCAATCTGAAGCTGGCGATTAGATGCAAGAAAAAGT 155
 ThrGlnAlaLysGlnThrAsnLeuGlnSerGluAlaGlyAspLeuAspAlaArgLysSer
 AGCGCTTCAAGCCCGAAACCCGCGCATTACTCGCTACTAACAGACAGTACTCGGGAGACAC 215
 SerAlaSerSerProGluThrArgAlaLeuLeuAlaThrLysThrValLeuGlyArgHis
 AAGATAGAGGTTCCGGCTTTGGAGGGTGGTTCAAAAGAAATCATCTAACGACAGAC 275
 LysIleGluValProAlaPheGlyGlyTrpPheLysLysSerSerLysHisGluThr
 GlyGlySerSerAlaAsnAlaAspSerSerSerValAlaSerAspSerThrGluLysPro 335
 TTGTTCCGTCTCACGCACGTTCTACGTATCCAAGGTAATGAGCGAATGGGATGTTGG 395
 LeuPheArgLeuThrHisValProTyrValSerGlnGlyAsnGluArgMetGlyCysTrp
 TATGCCCTGCGCAAGAATGGTTGGCCATTCTGTCGAAGCTGGCCTCGCCTAGGGCTGCCG 455
 TyrAlaCysAlaArgMetValGlyHisSerValGluAlaGlyProArgLeuGlyLeuPro
 GAGCTCTATGAGGGAAAGGGAGGCCAGCTGGCTACAAGATTTTCAGATGTAGAAAGG 515
 GluLeuTyrGluGlyArgGluAlaProAlaGlyLeuGlnAspPheSerAspValGluArg
 TTTATTACAAATGAAGGATTAACCTGGTAGACCTCCAGACAATGAGAGATTTACACAC 575
 PheIleHisAsnGluGlyLeuThrArgValAspLeuProAspAsnGluArgPheThrHis

Fig. 3A

GAAGAGTTGGGTGCACTGTTGATAAGCACGGGCCGATTATTTGGGTGGAAAACTCCG 635
 GluGluLeuGlyAlaLeuLeuTyrLysHisGlyProIleIlePheGlyTrpLysThrPro

AATGACAGCTGGCACATGTCGGTCCTCACTGGTGTGATAAAAGAGACGTCGTCCATTACT 695
 AsnAspSerTrpHisMetSerValLeuThrGlyValAspLysGluThrSerSerIleThr

TTTCACGATCCCCGACAGGGGCCGACCTAGCAATGCCGCTCGATTACTTTAACAGCGA 755
 PheHisAspProArgGlnGlyProAspLeuAlaMetProLeuAspTyrPheAsnGlnArg

TTGGCATGGCAGGTTCCACACGCAATGCTCTACCGCTAACGTAAGTAGCAGGGTATCTCACGTG 815
 LeuAlaTrpGlnValProHisAlaMetLeuTyrArgEnd

GCGGCATCATGACAAGCCCATGATGCCGCCAGCAGCTACCTGAATGCCGTCTGGCTTTT 875

GGTCCCTATTGTCGTATCCGGAAAGATGACGTCAAAGAATCTGGCAAGAGCTTTCTTGCT 935

CGACTCCTCAGCTTCCGGATCGATCAGGTCGCTGCCAGAGCGCGCTTGTCCATGAGCAT 995

CTGCCACAGCTGCTGGTCATGGTGTCCTCAGCTAAAGGGATTTGACGACAACCATGCG 1055

CAACTGCCGTGCGATACGCTCGATCCTGAAGCCCCGGTGTCCATGGCAGCCCCAAGAA 1115

AAAGACATAGTTCGCCGCTGTGAGGTTGTAGCCTGTGCCGGCGGCCACCTGGTCCCGAT 1175

AAACACCCCTGCAGTCCGGATCCTGCTGGAAAGCATCAATCGCCTTCTGCCGCTTGGGG 1235

CGAGTCACTGCCACCAACGTCACGCACCCGACGCCAAGCTTGAGGCAGTGCTCCGCAA 1295

CGTGGCCACGGATTCCTGATACTCGCAGAAGAGGATCACCTGTCGTCGAC 1346

Fig. 3B

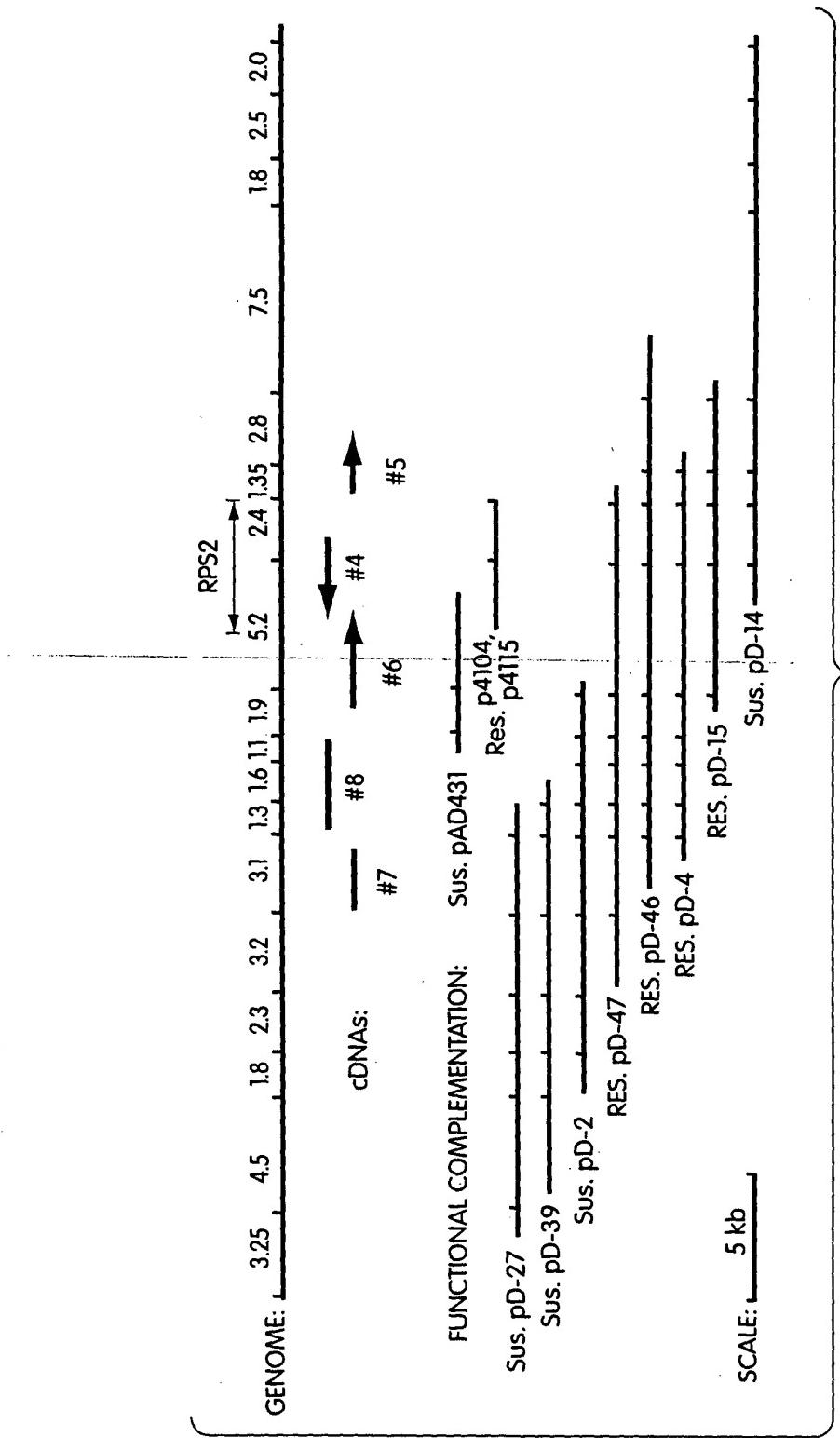


Fig. 4

1		50
L6pro	MSYLREVATA VALLLPFILL NKFWRPNSKD SIVNDDDDST SEVDAISDST	
Nprot	M
PrfP	
rps2	
51		6
L6pro	NPSGSFPSVE YE[VFLSFRGP DTREQFTDFL YQSLRRYKIM TFRDDDELK	
Nprot	ASSSSSSSRWS YD[VFLSFRGE DTRKTFTSHL YEVLNDKGKTFQDDKRLEY	
PrfP	LSKLDLIIID LKHQIESVKE
rps2	MDFISSLIVG CAQVLCESMN MAERRGHKTD LRQAITDLET	
101		150
L6pro	GKEIGPNLLR AIDQSKIYVP IISSGYADSK WCLMELAEIV RRQEEDPRRI	
Nprot	GATIPGELCK AIEESQFAIV VFSENYATSR WCLNELVKIM ECK.TRFKQT	
PrfP	GLLCLRSFID HFSESYDEHD	EA CGLIARVSVM AYKAE.....
rps2	AIGDLKAIRD DLTLRIQQDG LEGRSCSNRA REWLSAVQVT ETKTA.....	
151		7
L6pro	ILPIFYMVDP SDVRHQTGCY KKAFRKHANK F..DGQTIQN WKDALKKVGD	
Nprot	VIPIFYDVDP SHVRNQKESF AKAFEEHETK YKDDVEGIQR WRIALNEAAN	
PrfPYVIDS CLAYSHPLWY KVLW..... .IS..... .EVLENIKLV	
rps2LLLVR FRRREQRTM RRRY..... .LSCFGCAD YKLCKKKVSAI	
201		8 250
L6pro	LKGWHIGKND KQGAIADKVS ADIWHSISKE NLILE...TD ELVGIDDHIT	
Nprot	LKGSCDNRDK TDADCIRQIV DQISSKLCKI SLSY....LQ NIVGIDTHE	
PrfP	NKVVGETCER RNIEVTVHEV AKTTTYVAPS FSAYTQRANE EMEGFQDTID	
rps2	LKSIGELRER SEAICTDGGS IQVTCREIPI KSVVG..... NTTMM	
251		1 -P-loop
L6pro	AVLEKLSLDS ENVTMVGLYG MGGIGKTTA KAVYNKI... .SSC.FDCC	
Nprot	KIESLLEIGI NGVRIMGIWG MGGVGKTTIA RAIFDTLLGR MDSSYQFDGA	
PrfP	ELKDKLLGGS PELDVISIVG MPGLGKTTLA KKIYNDPEVT ..SRFDVHAQ	
rps2	EQVLEFLSEE EERGIIGVYQ PGGVGKTTLM QSINNELLTK ..G....HQY	
301		350
L6pro	CFIDNIRETQ EKDGVVVLQK KLVSEILRID ..SGS VGFNN DSGGRKTIKE	
Nprot	CFLKDIKE.. NKRGMHSLQN ALLSELLR.. .EKANYNN EEDGKHOMAS	
PrfP	CVVTQLYSWR EL.LLTILND VLEP...S.. .DRNEKED GE.IADELRR	
rps2	DVLIWVQMSR EF.GECTIQQ AVGA...RLG ..LSWDEKEF GENRALKIYR	
351		2
L6pro	RVSRFKILVV LDDVDEKFKF EDMLGSPKDF ISQ.SRFIIT SRSMRVLGTL	
Nprot	RLRSKKVLIV LDDIDNKDHY LEYLAGDLDW FGNGSRIIIT TRDKHLI...	
PrfP	FLLTKRFLIL IDDVWDYKWW DNLCMCFSD. VSNR SRIILT TRLNDVAEYV	
rps2	ALRQKRFLLL LDDVWEIDL EKTGVPRPD. RENKCKVMFT TRSIALCNNM	
		3
		400

Fig. 5A-1

401

450

L6pro NEN.QCKLYE VGSMSKPRSL ELFSKHAFKK NT....PPSY YETLANDVVD
 Nprot .EK.NDIIYE VTALPDHESI QLFQHQAFGK EV....PNEN FEKLSLEVNN
 PrfP .KC.ESDPHH LRLFRDDESW TLLQKEVFQG E....SCPPE LEDVGFEISK
 rps2 .GA.EYK.LR VEFLEKKHAW ELFCSKVWRK DLLESSSIRR LAEI...IVS

451 4

500

L6pro TTAGLPLTLK VIGSLLFKQE IAV..WEDTL EQL....RRT LNLDEVYDRLL
 Nprot YAKGLPLALK VNGSLLHNLR LTE..WKSAI EHM....KNN .SYSGIIDNV
 PrfP SCRGLPLSVV LVAGVLKQKK KTLD SWKVVE QSLs..SQRI GSLEESISII
 rps2 KCGGLPLALI TLGGAMAH.R ETEEEWIHAS EVLTRFFAEM KGMNYVFALL

501 5

9

550

L6pro KISYD ALNPE .AKEIFLDIA CFFIGQ..NK EEPYYMWTDC NFYPASNIIF
 Nprot KISYDG LEPK .QQEMFLDIA CFLRGE..EK DYILQILESC HIGAEYGLRI
 PrfP GFSYKNL.PH YLKPCFLYFG GFLQGKDIHD SKMTKLWVAE EFVQANN...
 rps2 KFSYDNLES D LLRSCFLYCA LFPEEHSIEI EQLVEYWVGE GFLTSSHGVN

551

10

600

L6pro LIQRCMIQVG DD DEFKMH DQLR DMGREIVRRE DVLPWKR SRI
 Nprot LIDKSLVFIS EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
 PrfP EK GQEDTRTRF. .LGRSYW...
 rps2 TIYKGYFLIG DLKAACLLET GDEKTQVKMH NVVRSFALWM ASEQGTYKEL

601

650

L6pro WSAAEGIDLL LNKKGSSKVK AISI.PWGVK YE FK.SECFL NLSELRYLHA
 Nprot WLAKVEEV M SNNTGT MAME AIWVSSYSST LRFS.NQAVK NMKRLRVFN M
 PrfP
 rps2 ILVEPSMGHT EAPKAENWRQ ALVISLLDNR IQTL.PEKLI CPKLTTLMQ

651

700

L6pro REAMLTGDFN NLLPNLK WLE LPFYKHGEDD PPLTNYTMKN LII.VILEHS
 Nprot GRSSTHYAID YLPNNLRCFV CTNYPW...E SFPSTFELKM LVH.LQLRH.
 PrfP
 rps2 QNSSLKKIPT GFFMHMPVLR VLDLSF.... TSITEIPLSI KYL. VELYHL

701

750

L6pro HITADDWGGW RHMMKMAERL KVVR LASNYS LYGR RVR...
 Nprot NSL RHLWTETKHL PSL..... RRID...
 PrfP
 rps2 SMSGTKISVL PQELGNLRKL KHLDLQRTQF LQTIPRDAIC WLSKLEVNL

751

800

L6pro .LSD.CWRFP KSIEVLSMTA IEMDEV DIGE LKKLKTLVLK FCPIQKISGG
 Nprot .LSW.SKRLT RTPDFTGM PN LEY..VNLYQ CSNLEEVHHS LGCCSKVIGL
 PrfP
 rps2 YY SY.AGWEL QSFG EDEAEE LGFADLEYLE NL TTLGITVL SLET LKTLFE

Fig. 5A-2

801	850
L6pro TFGMLKGLRE L.CLEFNWGT NLREVVADIG QLSSLKVILKT TGAKEVEINE	
Nprot YLNDCKSLKR F.....	PCVNVESLE
PrfP
rps2 FGALHKHIQH L.HVEECNEL LYFNLPSLTN HGRNLRRLSI KSCHDLEYLV	
851	900
L6pro FPLGLK.... .ELSTSSR IPNLSQLLDL EVLKVYDCKD GFDMPPASPS	
Nprot Y.LGLR.... .SCDSLEK LPEIYGRMKP EI..... QIHMQGSGIR	
PrfP
rps2 TPADFENDWL PSLEVTLHS LHNLTWRWGN SVSQDCLRNI RCINISHCNK	
901	950
L6pro EDESSVWWKV SKLKSLQLEK TRINVNVDD ASSGGHLPY LLPTSLTYLK	
Nprot ELPSSIFQYK THVTKL.. .WNMKNLVAL PSSICRL... .KSLVSLS	
PrfP
rps2 LKNVSWVQKL PKLEVIELFD CREIEELISE HESPSVEDPT LFP.SLKTLR	
951	1000
L6pro IYQCTEPTWL P.GIENLENL TSLEVNDIFQ TLGGDLDGLQ GLRSLEILRI	
Nprot VSGCSKLESL PEEIGDLDNL RVFDASDTL.	ILRP
PrfP
rps2 TRDLPELNSI LPSRFSFQKV ETLVITNCPR VKKLPFQERR TQMNLPTVYC	
1001	1050
L6pro RKVNGLARIK GLKDLLCSST CKLRKFYITE CPDLIELLPC ELGGQTVVVP	
Nprot P..... SSI IRLNKLIILM FRGFKDGVHF EFPPVAEGLH	
PrfP
rps2 EEKWWKALEK DQPNEELCYL PRFVPN....	
1051	1100
L6pro SMAELTIRDC PRLEVGPMLR SLPKFPMKK LDLAVANITK EEDLDAIGSL	
Nprot SLEYLNL.SY CNLIDGGLPE EIGSLSSLKK LDLSRNNF.. EHPSSIAQL	
PrfP
rps2
1101	1150
L6pro EELVSLELEL DDTSSGIERI VSSSKLQKLT TLVVKVPSLR EIEGLEELKS	
Nprot GALQSLDLK. DCQRFLTQLP ELPPELNELH .VDCHMALKF	
PrfP
rps2
1151	1200
L6pro LQDLYLEGCT SLGRLPLEKL KE.....LD IGGCPDLTEL VQTVVAVPSL	
Nprot IHDL.VTKRK KLHRVKLDDA HNDTMYNLFA YTMFQNISSM RHDISASDSL	
PrfP
rps2

Fig. 5A-3

1201	1250
L6pro RGLTIRDCPR LEVGPMIQLPKFPMNLNELT LSMVNITKED ELEVLSLEE	
Nprot .SLTV..... FTGQPYPEKI PSWFHHQGWD .SSVSVNLPE NWYIPDKFLG	
PrfP	
rps2	
1251	1300
L6pro LD.SLELTLD DTCSSIERIS FLSKLQKLTT LIVEVPSLRE IEGLAELKSL	
Nprot FAVCYRSRLI DTTAHLIPVC .DDKMSRMTQ KLALSECDTE SSNYSEWD.I	
PrfP	
rps2	
1301	1350
L6pro RILYL..... EGCTSLERL WPDQQQLGSL KNLNVLDIQG	
Nprot HFFFVVFAGL WDTSKANGKT PNDYGIIRLS FSGEEKMYGL RLLYKEGPEV	
PrfP	
rps2	
1351	1387
L6pro CKSLSVDHLS ALKTTLPRA RITWPDQPYR	
Nprot NALLQMRENS NEPTEHSTGI RRTQYNNRTS FYELING	
PrfP	
rps2	

Fig. 5A-4

6

N 2 ASSSSSSRWSYDVFLSFRGEDTRKTFSHLYEVLNQDKGIKTFQDDKRLEY 51
..|.|..|.:|..|.:|..|..|..|..|..|..|..|..|..|..|..|..|.
L6 51 NPSGSFPSVEYEVFLSFRGPDTREQFTDFLYQLSLRRYKIMTFRDDDDELLK 100
.
N 52 GATIPGELCKAIEESQFAIVVFSENYATSRWCLNELVKIMECK.TRFKQT 100
|..|...|.:|::|..:|..|.:|..|..|..|..|..|..|..|..|..|..|.
L6 101 GKEIGPNLLRAIDQSKIYVPIISSGYADSKWCLMELAEIVRRQEEDPRRI 150
7.
N 101 VIPIFYDVPDSHVRNQKESFAKAFEEHETKYKDDVEGIQRWRIALNEAN 150
::|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|.
L6 151 ILPIFYMVDPDSVRHQTCYKKAFRKHANKF..DGQTIQNWKDALKKVGD 198
8.
N 151 LKGSCDNRDKTADCIRQIVDQISSKLCKISLSY.LQNIVGIDTHLEKIE 199
|||..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|.
L6 199 LKGWHIGKNDKQGAIADKVSADIWSHISKENLILETDELVGIDDHITAVL 248

Fig. 5B-1

N 539 SSSLRFSNQAVKNMKRLRVFNMGRSSTHYAIIDYLPPNNLRCFVCTNYPW.. 586
: .. | .. . | :: || :
L6 591 GVKYEFKSECFLNLSELRYLHAREAMLTGDFNNLLPNLKWLPELFYKHGE 640
.
N 587 .ESFPSTFELKMLVHLQLRH.....NSLRHLWTETKHLPLSL..... 621
.
L6 641 DDPPLTNYTMKNLIIIVILEHSHITADDWGGWRHMMKMAERLKVVRLASNY 690
.
N 622RRIDLWSKRLTRTPDFTGMPNLEY..VNLYQCSNLEEVHHSLGCC 665
.
L6 691 SLYGRRVRLSDCWRFPKSIEVLSMTAIEDVDIGELKKLKTIVLKFPCI 740
.
N 666 SKVIGLYLNDCKSLKRFFPCVNVESLEYLGLRSCDSLEKLPEIYGRMKP.. 713
.
L6 741 QKISGGTFGMLKGLREL.....CLEFNWGTNLREVVADIGQLSSLK 781
.
N 714EIQIHMQGSGIRELP.SSIFQYKTHVTKLLLWNM....KNLV 750
.
L6 782 VLKTTGAKEVEINEFPLGLKELSTSSRIPNLSQLLDLEVVKVYDCKDGFD 831
.
N 751 ALPSSICRLKSLVSLSVSGC^{SKLES}SKLES^{LP}EEIGDLDNLRVFDASDTLILRP. 799
.
L6 832 MPPASPSEDESSVWWKV...SKLKSLQLEKTRINVNVDDASSGGHLPY 878
.
N 800PSSIIRLNKLIILMFRGFKDGVHFEPFPVAE 830
.
L6 879 LLPTSLTYLKIYQCTEPTWLPGIENLENLTSLEVNDIFQTLGGDLDGL.Q 927
¹².
N 831 GLHSLEYLNLSYCNLID..GGLPEEI.GSLSSLKKLDL..SRNNFEHLP^S 875
.
L6 928 GLRSLEILRIRKVNGLARIKGKDLCSTSCKLRKFYITECPDLIELLPC 977
.
N 876 SIA....QLGALQSLDLKDCQRLTQLPELPP^ELNELHVDC^HMALKFIHYL 921
.
L6 978 ELGGQTVVVPSMAELTI^RDCPRL.EVGPMIRSLPKFPM.....LKKLDLA 1021
.
N 922 VTKRKKLHRVKLDDAHNTMYNLFAYTMFQNISSMRHDISASDSL^LTVF 971
.
L6 1022 VANITKEEDLDAIGSLEELV..SLELELDDTSSGIERIVSSSKLQKL^TTL 1069
.
N 972 TGQPYPEKIPSWFHHQGDSSVSVN.....LPENWYIPDKFLGF^AVCY 1014
.
L6 1070 VV.....KVPSLREIEGLEELKSLQDLYLEGCTS^LGRLPLEKL^KELD^IGG 1114
. .

Fig. 5B-2

N 1015 SRSLIDTTAHLIPVCDDK.....MSRMTQKLA...LSECDTES 1049
...|.. .: .. ::|.. : ..|.: ..|.|.: ..|..| ..
L6 1115 CPDLTELVQTVVAVPSLRGLTIRDCPRLEVGPQMIQSLPKFPMLNELTLSM 1164

N 1050 SNYSEWDIHFFFVVPFAGLWDTSKANGKTPNDYGIIRLSFSGEEKMYGLRL 1099
|... | ..:::| . . . :|....:|.. :| :|: .| :
L6 1165 VNITKEDELEVLGSLEELDSLELTLDTCSSIERISF.LSKLQKLTLIV 1213

N 1100 LYKEGPVNALLQMRENSNEPTEHSTGIRRTQYNNRTSFYELIN 1143
.. .|:::| ::: . | :|::| : .. : .| |
L6 1214 EVPSLREIEGLAELKSLRILYLEGCTSler.LWPDQQQLGSLKN 1256

Fig. 5B-3

<p>ATCGATTCTCATCTTATCGTGGCTGCTCACCGCTGTGAACTATGATAATGCCGACAGAACATAAGACISACTTAGACAAGCCATCACTGACTTGAAAC</p> <p>M D F I S S L I V G C A Q V L C E S M N M A E R R G H K T D L R Q A I T D L E T</p> <p><u>I G D L K A I R D D L T L R I Q Q D G L E G R S C S N R A R E W L S A V Q V T</u></p> <p>A I G D L K A I R D D L T L R I Q Q D G L E G R S C S N R A R E W L S A V Q V T</p> <p>leucine-zipper</p>	<p>-32 ACAAGTAAAGAAGACCGAGAAATCATCGAA -1</p> <p>360 GAGACTAAACAGCCCTACTTTAGGAGCTTAGGGCGTGGGAACACAGGACGGAACTCAGGAGATACTCAGTTCTGGCTGCCCCACTACAACTGTGCAAGGAGTTCT</p> <p>120 E T K T A L L L V R F R R R E Q R T R M R R R Y L S C F G C A D Y K L C K K V S</p> <p>480 GCCATATTGAAAGAGCATGGTGGAGCTGAGAACAGCTCTGAAAGCTATCAAAACAGATGGGGTCATTCAAGTACTCTAGAGAGATAACCCATCAAGTCCGTGTCGAAATACCACG</p> <p>160 A I L K S I G E L R E R S E E A I K T D G G S I Q V T C R E I P I K S V V G N T T</p> <p>600 ATGATGAAACAGGTTTGGAAATTCTCAGTCAAAGAACAAAGAGGAACTATGGCTTATGGACCTCTGGGGTGGAAAGACAACGTTAATGCAGAGCTTAACAACGAGCTGATC</p> <p>200 M M E Q V L E F L S E E E R G I I G V Y G P G G V G K T L M Q S I N N E L I</p> <p>720 ACAGAAGACATCAGTATGATCTACTGATTGGCTCAAACTCCAGAGAAATTGGCCAGGTACAAATTGCAAGCCGTGGGACCCGTTATCTGGGACCAAGGAGAC</p> <p>240 T K G H Q Y D V L I W V Q M S R E F G E C T I Q Q A V G A R L G L S W D E K E T</p> <p>840 GCGGAAACAGAGCTTGAAGATAACAGACCTTGAGAGAGAACGTTCTCTGCTGCTAGATGATGCTGGGAAGAGATACTGGAGAAACTGGAGTCCCTGACAGG</p> <p>280 G E N R A L K I Y R A L R Q K R F L L L D D V W E E I D L E K T G V P R P D R</p> <p>kinase-2</p>
---	---

Fig. 6A

GAAACAAATGCCAAGGTGTTCACCGACACGGCTATA
 E N K C K V M F T T R S I A L C N N M G A E Y K L R V E F L E K K H A W E L F C 960
 320

ACTAACGATTCGAGAAAGACTTCTAGACTCATCATCAATTGGCCGCTGGGAGATTACTGAGTAATGGAGATTCCACTAGCTGATCATTAGCAGGCCATTG
 S K V W R K D L L E S S S I R R L A E I I V S K C G G L P L A L I T L G G A M A 1080
 360

kinase-3a

membrane integrated

CATAAGAGACAGAGAGAGCTGATCCATGACTGAAGTCTGACTAGATTCAGAGAGATGAAGGTATGAACTATGATATTGCCCTTGAAATTGAGCTACGACACCTCGAG 1200
 H R E T E E W I H A S E V L T R F P A E M K G M N Y V F A L L K F S Y D N L E 400

AGTGATCTGCTTCGGCTCTCTCTGACTGGCCTTAATTCCAGAAGAACATCTATAGAGATGAGCAGCTGTTGACTACTGGCTGGCGAACGGTTCTCACCGCTCCATGCG 1320
 S D L L R S C F L Y C A L F P E E H S I E I E Q L V E Y W V G E G F L T S S H G 440

GTAAACACCATTACAAGGGTATTCTCATGGGACTCTGAAACGGGACTGTTGAAACGGACATGAGAACACGGTGAGATGATAATGGCTCAGAACGGTTCTCACCGCTCCATGCG 1440
 V N T I Y K G Y F L I G D L K A A C L L E T G D E K T Q V K M H N V V R S F A L 480

TGGATGGCATCTGACAGGGACTTATAAGGGCTGATCCAGTTGAGCCTAGCATGGGACATACTGAAGCTCTTAAGGAGAAACTGGCACAAGGGTTGGTGCATCTATGTTAGAT 1560
 W M A S E Q G T Y K E L I L V F P S M G H T E A P K A E N W R Q A L V I S L L D 520

AACAGAAATCCAGAACCTTGCTGAAAAACTCATATGCCGAAACTGACAACTGATGCTCCAAACAGAACAGCTCTTGAGAGATCCAAACAGGTTTCATGCCATATGCCCTGTTCTC 1680
 N R I Q T L P E K L I C P K L T T L M L Q Q N S S L K K I P T G F F M H M P V L 560

AGAGCTCTGGACTTGTGCTTCAAGTATCTGAGATTCCTGTTCTAAGTATTGGAGTTGATCATCTGCTCTATGAGAACAAAGATAAGTGTATGCCACAGGAGCT 1800
 R V L D L S F T S I T E I P L S I K Y L V E L Y H L S M S G T K I S V L P Q E L 600

Fig. 6B

GGGAACTTAGAAACTGAAGCTCGGACCTACAAAGAACCTCAGTTCTCAGACGATCCACCGAGATGCCATATGTGCGCTGAGAACGTCGAGGTCTCAACTGTACTACATAC 1920
 G N L R K L K H L D L Q R T Q F L Q T I P R D A I C W L S K L E V L N L Y Y S Y 640

 GCGGGTGGAACTGCAGAGCTTGGAGAAGATGAGCAGAAGAACCTGGATTGGCTCACTGGAAACTAACACACTGGTATCATCTCTCATGGAGACCTA 2040
 A G W E L Q S F G E D E A E E L G E A D L E Y L E N L T T L G I T V L S L E T L 680

 AAAACTCTCTCGAGTCGGTCTTCGATAAACATATAACGATCTCACCGTGAGAGTGCAATGAACTCTCTACTCACTCCACATCACTCACTAACATGGCAGGACCTGAGA 2160
 K T L F E F G A L H K H I Q H L H V E E C N E L L V F N L P S L T N H G R N L R 720

 AGACTTACCATAAAGTGGCATGACTTGGAGTACCTGGTCACACCCGAGATTCAAATGATGGCTCCGAGCTAGAGGTCTCACGTTACACCCCTCACAACTAACAGGA 2280
 R L S I K S C H D L E Y L V T P A D F E N D W L P S L E V L T L H S L H N L T R 760

 GTGTGGCAAATCTGTAAGCCAGATGCTCGGAAATACCGTCTGCATAAACATTCACACTGCAACAAGCTGAAGAATGTCATGGCTCAGAAACTCCAAAGCTAGAGGTGAT 2400
 V W G N S V S Q D C L R N I R C I N I S H C N K L K N V S W V Q K L P K L F V I 800

 GAACCTGTCGACTGCAGAGAGATAGAGGAATGATAACGCCAACACGGAGTCCATCCCTCGAAGATCCAACATGTTCCAAAGCCTGAACACCTTGAGAACACTAGGGATCTCCAGAACTA 2520
 E L F D C R E I E E L I S E H E S P S V E D P T L F P S L K T L R T R D L P E L 840

 AACAGCATCTCCCCATCTGATTTCATCCAAAAGTGGAAACATPAGCATCACAAATGCCAGGTTAAGAAACTGGCTTCAGGAGGGAGCCAGATGAACATGGCAACCA 2640
 N S I L P S R F S F Q K V E T L V I T N C P R V K K L P F Q E R R T Q M N L P T 880

Fig. 6C

GTTTATGTGAGGAGAAATGGTGAAGCAGTGAAAGATCAACCAACGAGCTTGTATTACCGCCCTTGTCCAATTTGATAAGAGCTAAGACCACITGTACAATA 2760
V Y C E E K W W K A L E K D Q P N E E L C Y L P R F V P N * 909

TGTCCATTCATAAGTAGCAGGAAGCCAGGAGGTGTCCACTGAACTCATCACTTCCACTAGACCAAAACTAGAGATTATGTAATCATAAAACCAAACATCCGGATCAATA 2880

GATCTCACGACTATGAGGAGCAGACTCACCGAGTATCGTCCATATAGAAACTCCAACTCCAGTCCAGTCAGTGAGAACGAACTTATCAGATCTCTGAAACAAATTCTGGAAATC 3000

GTCACCTCAGATTAGACCTCCAGTAAGAAGTGAGAACGATGACCGACACTGTGAAAGAATTGAGCTAATGAGCTGAAACCGATCCGGTAAATGCAGAACCGGATCCGGAGAGAA 3120

TTTGCATTGTGATCTTATTTAATTTGAGCCCCAAATACTAGATATGTAGTGAGACCAAACTCATGATCAATGTTCAATTTCGTAG 3240

TGTAATAACGGAAAGGATAAAAGGTCACTGAGT (A)_n

Fig. 6D

consensus **PXXaXX LXXLXXXLXaXXXX aXXa**

505	P KAENW RQALVISLLD NR IQTL	
527	P EKLIC PK L T T MLQQNSSLKKI	
550	P TGFFMHMPVLRVLDLSFTS I TEI	
574	P LSIKY LVELYHLSMSGTK I SVL	
597	P QELGN LRKLKHLDLQRTQFLQTI	
621	P RDAICWLSKLEVNLYYSYAGWEL	QSFGEDAEELG
658	F ADLEY LENLT T LGITVLS L ETL	KT
683	L FEFGALHKHIQHLHVEECNELLYF	NL
710	P SLTNHGRNLRRRLSIKSCHDLEYL	VT
736	P ADFENDWLP S LEVLT L HSLHN L TRV	WGN
765	S VSQDC LRNIRCINISHCNKLN V	SWVQKL
795	P K L EV IELFD C REIEELISEHES	PSVED
823	P T LFPSL K TLR R D L PELNSI L	
845	P SRFS FQKVETLVITNCPRVKL	

Fig. 7

MDFTISSLIVG CAQVLCESMN MAERRGHKID LROAQTDLER AIGDIKAIRD DITLRIQQDG 60
 LEGRSCSNRA REWLSAVQVT ETKTALLVR FRRREORTRM RRRYLSCFGC ADYKLCKKVS 120
 AIUKSIGELR ERSEAIKTDG GSIQVTCREI PIKSUVGNTT MMEQVLEFLS EEEERGIIGV
P loop 180
YGRGGVGKTT LMQSINNVELI TKGHQYDVL LI WVQMSREFGE CTIQQAVGAR LGISWDEKET 240
 GENRALKIYR ALROKRFLLL LDDVWEIDL EKTGVPRPDR ENKCKVMFTT RSIALCNCNNMG
Membrane-spanning 360
 AEYKLVEFL EKKHAWELFC SKVWRKDILE SSSIRRRAEI IVSKCGGLPL ALITGGAMA 420
 HIRETEEEWIH ASEVLTRFPA EMKGMYVFA LLKF SYDNLE SDLRSCFLY CALFPEEHSTI
 EIEQIIVEYW GEGFLTSHG VNTIKGYFL IGDIIKAACIL ETGDEKTOVK MHNVRSFAL 480
 WMASEQGTYK ELLVEPSMG HTEAPKAENW RQALVISLD NRIQTLPEKL TCPKLTTLMI
 QONSSLKKIP TGFFMHMPVL RVLDLSFTSI TPIPLSIKYL VELYHLSMSG TKISVLQPQL 540
 GNLRKLIKHD LQRTQFLQT PRDATICWL SK LEVNLYSY AGWELQSFGEE DEAEELGFAD 600
 LEYLENLITL GITVLSLETI KTLFEFGALH KHIQHLHVEE CNELLYFNLP SLTNHGRNLR 660
 RLSTIKSCHDL EYLVTPADFE NDWLPNSLEV TLHSLHNLTR VWGNNSVSQDC LRNIRCTNIS 720
 (end Leucine-rich repeats) 780
 HCNKLNKVSW VOKLPKLEVI ELFDCREIEE LISEHESPSV EDPTLFPSSLK TIRTRDLPRL 840
 NSILPSRFSF OKVETLVITN CPRVKKLPO ERRTOMLP T VYCEEKWWKA LEKDDQPNELI 900
 CYLPRFVPM 909

Fig. 8

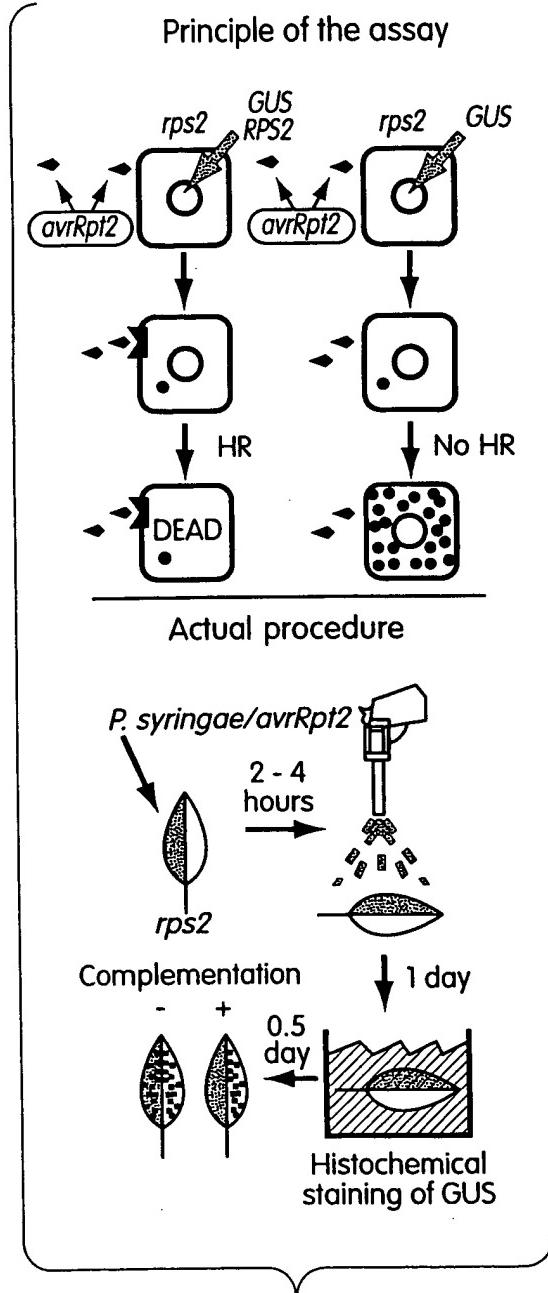
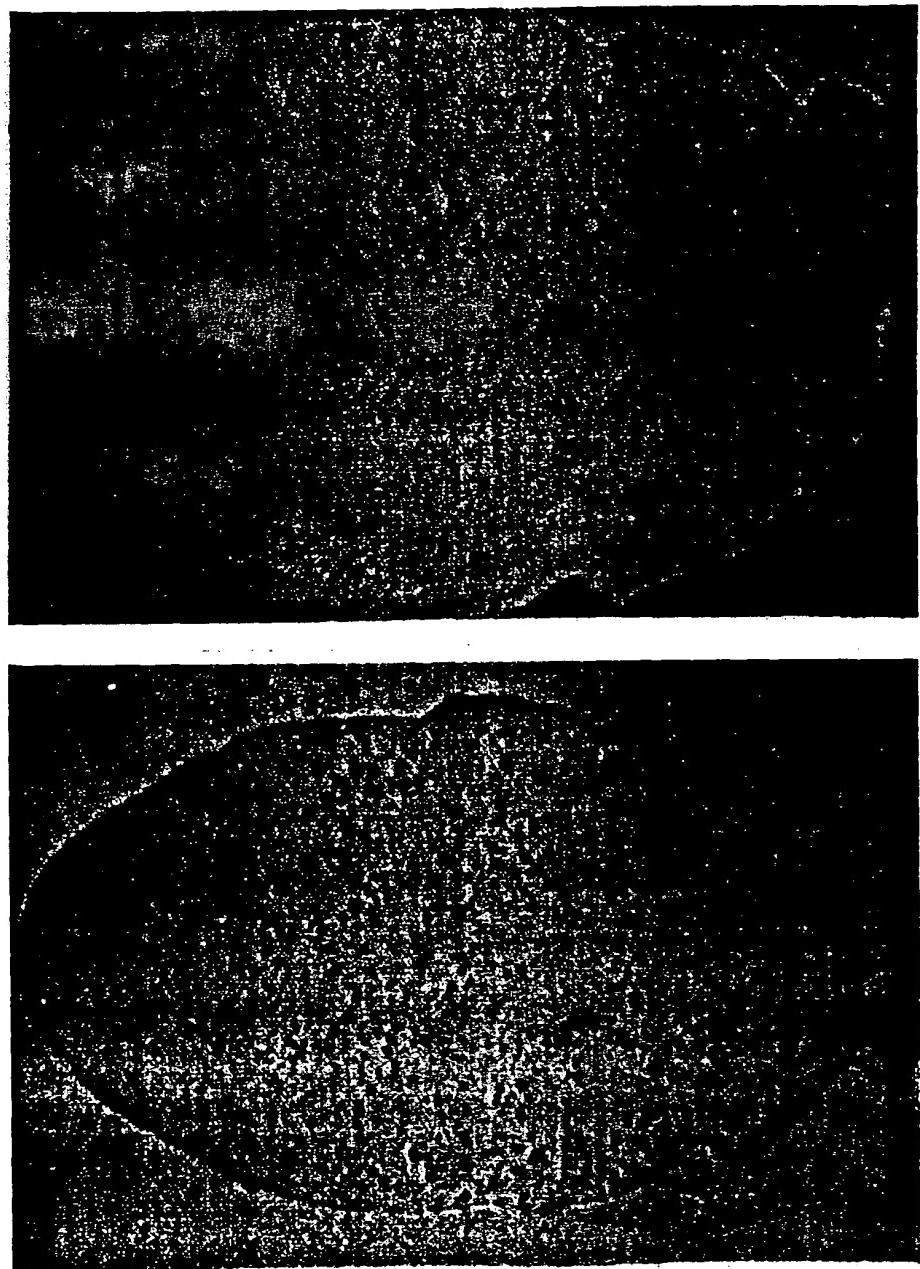


Fig. 9

Fig. 10A
Fig. 10B



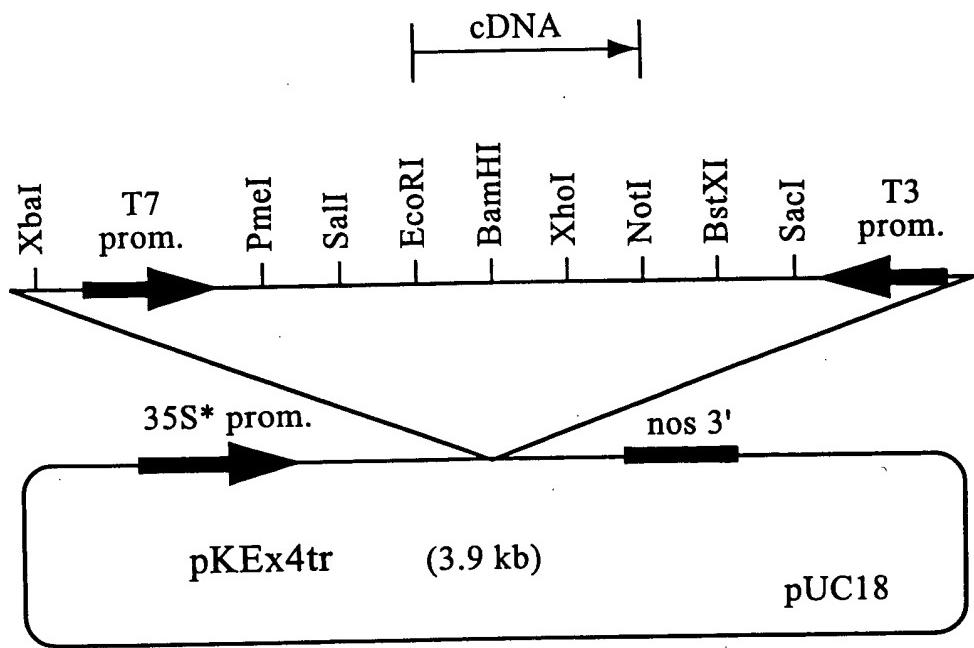


Fig. 11

	10	20	30	40	50	60
1	aagctttaca	gattggatga	tctcttaatg	catgctgaag	tgactgc当地	aaggtagca
61	atattcagt	gttctcgta	tgaatattc	atgaacgaa	gcagcactga	gaaaatgagg
121	cccttgat	ctgattttct	gcaagagatt	gagtctgtca	aggttagatt	cagaaatgtt
181	tgcttgcaag	ttctggat	atcaccttt	tcccgtacag	atggagaagg	ccttgttaat
241	ttcttattaa	aaaaccaggc	caaggtgccg	aatgatgtat	ctgttcttc	tgatgaaagt
301	tttagaggatg	caagcagcac	tgagaaaaatg	ggacttccat	ctgatattct	ccgagagatt
361	gagtctgtt	agataaagga	ggccagaaaa	ttatatgatc	aagtttgg	tgcaacacat
421	tgtgagacga	gtaagcacga	tggaaaagc	tttatcaaca	ttatgttaac	ccaacaggac
481	aaggtgctgg	actatgtgc	tggttcgt	tcttatcttc	ttaaccaa	ctcagtagtt
541	aaagacaaaa	tattgcacat	tggcttta	ctttagata	ttgtacagta	ccgaaatatg
601	catatagaac	ttacagatct	cgctgaacgt	gttcaagata	aaaactacat	tcgttcttc
661	tctgtcaagg	gttatattcc	tgcttggtat	tacacactat	atctctctga	tgtcaagcaa
721	ttgcttaagt	ttgttgaggc	agaggtaaag	attatttgc	tgaaagtacc	agattcttca
781	agttatagct	tccctaagac	aaatggatta	ggatatctca	attgttttt	aggcaaattg
841	gaggagctt	tacgttctaa	gctcgattt	ataatcgact	taaaacatca	gattgaatca
901	gtcaaggagg	gcttatttgc	cctaagatca	ttcattgatc	attttcaga	aagctatgtt
961	gagcatgatg	aagttgtt	tcttata	agagttctg	taatggcata	caaggctgag
1021	tatgtcattt	actcatgtt	ggcctattt	catccactct	ggtacaaaat	tctttggatt
1081	tctgaagttc	ttgagaat	taagcttga	aataaagtt	ttggggagac	atgtgaaaga
1141	aggaacactg	aagttactgt	gcatgaagtt	gcaaaagacta	ccactaatgt	agcaccatct
1201	ttttcagctt	atactcaaag	agcaaacgaa	gaaatggagg	gtttcagga	tacaatagat
1261	gaattaaagg	ataaaactact	tggaggatca	cctgagctt	atgtcatctc	aatcggttgc
1321	atgccaggat	tggcaagac	tacactagca	aagaagattt	acaatgatcc	agaagtcacc
1381	tctcgcttcg	atgtccatgc	tcaatgttt	gtgactcaat	tatattcatg	gagagagtt
1441	ttgctcacca	tttgaatga	tgtgcttgc	ccttctgatc	gcaatgaaaa	agaagatgga
1501	gaaatagctg	atgatctacg	ccgattttt	ttgaccaaga	gattttgtat	tctcattttat
1561	gatgtgtggg	actataaagt	gtgggacaat	ctatgtatgt	gcttcagtga	tgtttcaaat
1621	aggagtagaa	ttatccaaac	aaccgcgtt	aatgatgtcg	ccgaatatgt	caaatgtgaa
1681	agtatcccc	atcatctcg	tttattcaga	gatgacgaga	gttggacatt	attacagaaa
1741	gaagtcttc	aaggagagag	ctgtccacat	gaacttgaag	atgtggatt	tgaaatatca
1801	aaaagttgt	gagggttgc	tctctcgtt	gtgttagat	ctgggttct	gaaacagaaa
1861	aagaagacac	tagattcatg	gaaagtagta	gaacaaatgc	taagttccca	gaggatttgc
1921	acgttggaaag	agagcatatc	tataatttga	ttcagttaca	agaatttacc	acactatctt
1981	aagccttgc	ttctctattt	tggaggattt	ttgcaggaa	aggatattca	tgactcaaaa
2041	atgaccaagt	tgtggtagc	tgaagatgtt	gtacaagaa	acaacgaaaa	aggacaagaa
2101	gatacccgca	caaggtttct	tggacgtat	tattggtagg	aatctgttga	tggccatgga
2161	gaagagacat	aatgccaagg	tggaaacgtt	ccgcattat	gatttgc	ataaaattctg
2221	catggaaaag	gccaaacaag	aggatccct	tctccagatc	aatagttaaa	aaaaactgt
2281	ttaatttac	attacaaaaa	aaaagaactg	tattaattt	actgtattat	gtttatgcca
2341	actctcattt	ccatgtgtt	tctttattt	aattcagtgg	agaaggtgt	tttcctgaac
2401	gattgaaaga	ataccgattt	ttcggttatt	cttaccaaga	tgaaattgtat	ctgtggcgcc
2461	catctcgctc	taatgtccgc	tcttactat	tcaatgcata	tgatccagat	aacttgc当地
2521	ggccgcgtga	tatctccttc	attttgaga	gcttcaagct	tgtaaagtg	ttggattttgg

Fig. 12A

Fig. 12B